

10/561092

034123-109_ST25.txt
SEQUENCE LISTING
JAP200301PCT/PTO 16 DEC 2005

<110> THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
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WADIA, Jehangir S

<120> POLYPEPTIDE TRANSDUCTION AND FUSOGENIC PEPTIDES

<130> 034123-109

<140> PCT/US2004/20837

<141> 2004-06-18

<150> 60/480,065

<151> 2003-06-20

<160> 21

<170> PatentIn version 3.3

<210> 1

<211> 86

<212> PRT

<213> Unknown

<220>

<223> transducing protein

<400> 1

Met Glu Pro Val Asp Pro Arg Leu Glu Pro Trp Lys His Pro Gly Ser
1 5 10 15

Gln Pro Lys Thr Ala Cys Thr Asn Cys Tyr Cys Lys Lys Cys Cys Phe
20 25 30

His Cys Gln Val Cys Phe Ile Thr Lys Ala Leu Gly Ile Ser Tyr Gly
35 40 45

Arg Lys Lys Arg Arg Gln Arg Arg Arg Pro Pro Gln Gly Ser Gln Thr
50 55 60

His Gln Val Ser Leu Ser Lys Gln Pro Thr Ser Gln Ser Arg Gly Asp
65 70 75 80

Pro Thr Gly Pro Lys Glu
85

<210> 2

<211> 20

<212> PRT

<213> Unknown

<220>

<223> HA2 analog

<400> 2

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Gly Gly Trp Thr Gly
1 5 10 15

Met Ile Asp Gly
20

<210> 3
<211> 20
<212> PRT
<213> Unknown

<220>
<223> HA2 analog

<400> 3

Gly Leu Phe Glu Ala Ile Ala Glu Phe Ile Glu Gly Gly Trp Glu Gly
1 5 10 15

Leu Ile Glu Gly
20

<210> 4
<211> 5
<212> PRT
<213> Unknown

<220>
<223> linker moiety

<400> 4

Gly Gly Gly Gly Ser
1 5

<210> 5
<211> 6
<212> PRT
<213> Unknown

<220>
<223> linker moiety

<220>
<221> Xaa
<222> (6)..(6)
<223> Xaa = any number of repeats of amino acids 1-5

<400> 5

Gly Gly Gly Gly Ser Xaa
1 5

<210> 6
<211> 12

<212> PRT
 <213> Unknown

<220>
 <223> linker moiety

<400> 6

Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Ser
 1 5 10

<210> 7
 <211> 14
 <212> PRT
 <213> Unknown

<220>
 <223> linker moiety

<400> 7

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Lys Gly
 1 5 10

<210> 8
 <211> 18
 <212> PRT
 <213> Unknown

<220>
 <223> linker moiety

<400> 8

Gly Ser Thr Ser Gly Ser Gly Lys Ser Ser Glu Gly Ser Gly Ser Thr
 1 5 10 15

Lys Gly

<210> 9
 <211> 18
 <212> PRT
 <213> Unknown

<220>
 <223> linker moiety

<400> 9

Gly Ser Thr Ser Gly Ser Gly Lys Pro Gly Ser Gly Glu Gly Ser Thr
 1 5 10 15

Lys Gly

<210> 10

<211> 14
 <212> PRT
 <213> Unknown

<220>
 <223> linker moiety

<400> 10

Glu Gly Lys Ser Ser Gly Ser Gly Ser Glu Ser Lys Glu Phe
 1 5 10

<210> 11
 <211> 30
 <212> PRT
 <213> Unknown

<220>
 <223> HA2 TAT peptide

<400> 11

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly
 1 5 10 15

Met Ile Asp Gly Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
 20 25 30

<210> 12
 <211> 20
 <212> PRT
 <213> Unknown

<220>
 <223> HA2 peptide

<400> 12

Gly Leu Phe Gly Ala Ile Ala Gly Phe Ile Glu Asn Gly Trp Glu Gly
 1 5 10 15

Met Ile Asp Gly
 20

<210> 13
 <211> 418
 <212> DNA
 <213> Unknown

<220>
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<400> 13
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 gagcggataa caattcccct ctagaaataa ttttgtttaa ctttaagaag gagatatacc 120
 atgggcagca gccatcatca tcatcatcac agcagcggcc tggcgccgcg cggcagccat 180

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atgaggaaga agcggagaca gcgacgaaga ggctcggatc cgaattcgag ctccgtcgac	240
aagcttgcgg ccgcactcga gcaccaccac caccaccact gagatccggc tgctaacaaa	300
gcccgaaggg aagctgagtt ggctgctgcc accgctgagc aataactagc ataaccctt	360
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<210> 14
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 <212> DNA
 <213> Unknown

<220>
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<400> 14 cgcattctct agctctagag ctagggcgct ttaattatgc tgagtgatat ccccttaaca	60
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taccgcgtcg cggtagtagt agtagtagtg tcgtcgccgg accacggcgc gccgtcggta	180
tactccttct tcgcctctgt cgctgcttct ccgagcctag gcttaagctc gaggcagctg	240
ttcgaacgcc ggcgtgagct cgtggtggtg gtggtggtga ctctaggccg acgattgttt	300
cgggctttcc ttcgactcaa ccgacgacgg tggcgactcg ttattgatcg tattggggaa	360
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<210> 15
 <211> 53
 <212> PRT
 <213> Unknown

<220>
 <223> TAT peptide

<400> 15

Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His Met Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly Ser
20 25 30

Asp Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu Glu His
35 40 45

His His His His His
50

<210> 16
 <211> 360
 <212> DNA

<213> Unknown

<220>

<223> cDNA

<400> 16

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atgggcagga agaagcggag acagcgacga agaggccata tggctagcat gactggtgga      180
cagcaaatgg gtcgggatcc gaattcgagc tccgtcgaca agcttgcggc cgcactcgag      240
caccaccacc accaccactg agatccggct gctaacaaag cccgaaagga agctgagttg      300
gctgctgcca ccgctgagca ataactagca taacccttg gggcctctaa acgggtcttg      360

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<210> 17

<211> 360

<212> DNA

<213> Unknown

<220>

<223> cDNA

<400> 17

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taccgcctct tcttcgcctc tgctcgctgct tctccggtat accgatcgta ctgaccacct      180
gtcgtttacc cagccctagg cttaagctcg aggcagctgt tcgaacgccg gcgtgagctc      240
gtggtggtgg tgggtggtgac tctaggccga cgattgtttc gggctttcct tcgactcaac      300
cgacgacggt ggcgactcgt tattgatcgt attggggaac cccggagatt tgcccagaac      360

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<210> 18

<211> 46

<212> PRT

<213> Unknown

<220>

<223> TAT peptide

<400> 18

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Met Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly His Met Ala Ser
1           5           10           15

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Met Thr Gly Gly Gln Gln Met Gly Arg Asp Pro Asn Ser Ser Ser Val
          20           25           30

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Asp Lys Leu Ala Ala Ala Leu Glu His His His His His His
35           40           45

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<210> 19
 <211> 1437
 <212> DNA
 <213> Unknown

<220>
 <223> cDNA

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 ttttgtttaa ctttaagaag gagatatacc atgggcagga agaagcggag acagcgacga 180
 agaggccata tggctagcat gactggtgga cagcaaatgg gtcgggatcc gaattccatg 240
 tccaatttac tgaccgtaca ccaaaatttg cctgcattac cggtcgatgc aacgagtgat 300
 gaggttcgca agaacctgat ggacatgttc agggatcgcc aggcgttttc tgagcatacc 360
 tggaaaatgc ttctgtccgt ttgccggtcg tgggcggcat ggtgcaagtt gaataaccgg 420
 aaatggtttc ccgcagaacc tgaagatgtt cgcgattatc ttctatatct tcaggcgcg 480
 ggtctggcag taaaaactat ccagcaacat ttgggcccagc taaacatgct tcatcgtcgg 540
 tccgggctgc cacgaccaag tgacagcaat gctgtttcac tggttatgcg gcggatccga 600
 aaagaaaacg ttgatgccgg tgaacgtgca aaacaggctc tagcgttcga acgactgat 660
 ttcgaccagg ttcgttcact catggaaata gcgatcgctg ccaggatata cgtaatctgg 720
 catttctggg gattgcttat aacaccctgt tacgtatagc cgaaattgcc aggatcaggg 780
 ttaaagatat ctcacgtact gacggtggga gaatgttaat ccatattggc agaacgaaaa 840
 cgctgggttag caccgcagg ttagagaagg cacttagcct gggggtaact aaactggtcg 900
 agcgatggat ttccgtctct ggtgtagctg atgatccgaa taactacctg ttttgccggg 960
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 gatacctggc ctggtctgga cacagtgcc gtgtcggagc cgcgcgagat atggcccgcg 1140
 ctggagtttc aataccggag atcatgcaag ctggtggctg gaccaatgta aatattgtca 1200
 tgaactatat ccgtaacctg gatagtgaac caggggcaat ggtgcgccctg ctggaagatg 1260
 gcgatgcggc cgactcgag caccaccacc accaccactg agatccggct gctaacaaaag 1320
 cccgaaagga agctgagttg gctgctgcca ccgctgagca ataactagca taacccttg 1380
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<210> 20
 <211> 1438
 <212> DNA
 <213> Unknown

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<220>

<223> cDNA

<400> 20

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aaaacaaatt gaaattcttc ctctatatgg taccgcctct tcttcgcctc tgtcgctgct    180
tctccggtat accgatcgta ctgaccacct gtcgtttacc cagccctagg cttaagggtac    240
aggttaaatg actggcatgt ggttttaaac ggacgtaatg gccagctacg ttgctcacta    300
ctccaagcgt tcttggaacta cctgtacaag tccctagcgg tccgcaaaag actcgatatg    360
acctttttacg aagacaggca aacggccagc acccgccgta ccacgttcaa cttattggcc    420
tttaccaaag ggcgtcttgg acttctacaa gcgctaatag aagatataga actccgcgcg    480
ccagaccgtc atttttgata ggtcgttgta aaccgggtcg atttgtaga agtagcagcc    540
aggcccgacg gtgctgggtc actgtcgta cgacaaagt accaatacgc cgcctaggct    600
tttcttttgc aactacggcc acttgcacgt tttgtccgag atcgcaagct tgcgtgacta    660
aagctggtcc aagcaagtga gtacctttta tcgctagcga cggctctata tgcattagac    720
cgtaaagacc cctaacgaat attgtgggac aatgcataat ggctttaacg gtcctagtcc    780
caattttctat agagtgcatt actgccaccc tcttacaatt aggtataacc gtcttgcttt    840
tgcgaccaat cgtggcggtc acatctcttc cgtgaatcgg acccccattg atttgaccag    900
ctcgtacct aaaggcagag accacatcga ctactaggct tattgatgga caaacggcc    960
cagtcttttt taccacaacg gcgcggtaga cggtggtcgg tcgatagttg agcgcgggac   1020
cttcctaaa aacttcgttg agtagctaac taaatgccgc gattcctact gagaccagtc   1080
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tacttgatat aggcatgga cctatcactt tgtccccgtt accacgcgga cgaccttcta   1260
ccgctacgcc ggcgtgagct cgtgggtggtg gtgggtggtga ctctaggccg acgattggtt   1320
cgggctttcc ttcgactcaa ccgacgacgg tggcgactcg ttattgatcg tattggggaa   1380
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<210> 21

<211> 383

<212> PRT

<213> Unknown

<220>

<223> TAT peptide

<400> 21

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Met Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg Gly His Met Ala Ser
 1 5 10 15
 Met Thr Gly Gly Gln Gln Met Gly Arg Asp Pro Asn Ser Met Ser Asn
 20 25 30
 Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val Asp Ala Thr
 35 40 45
 Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg Asp Arg Gln
 50 55 60
 Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val Cys Arg Ser
 65 70 75 80
 Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe Pro Ala Glu
 85 90 95
 Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala Arg Gly Leu
 100 105 110
 Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn Met Leu His
 115 120 125
 Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala Val Ser Leu
 130 135 140
 Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly Glu Arg Ala
 145 150 155 160
 Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln Val Arg Ser
 165 170 175
 Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn Leu Ala Phe
 180 185 190
 Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu Ile Ala Arg
 195 200 205
 Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg Met Leu Ile
 210 215 220
 His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly Val Glu Lys
 225 230 235 240
 Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp Ile Ser Val
 245 250 255

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Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys Arg Val Arg
260 265 270

Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu Ser Thr Arg
275 280 285

Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile Tyr Gly Ala
290 295 300

Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly His Ser Ala
305 310 315 320

Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val Ser Ile Pro
325 330 335

Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile Val Met Asn
340 345 350

Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val Arg Leu Leu
355 360 365

Glu Asp Gly Asp Ala Ala Ala Leu Glu His His His His His His
370 375 380